REMARKS UNDER 37 CFR § 1.111

Formal Matters

Claims 1-56 and 80-90 and 92-101 are pending after entry of the amendments set forth herein.

Claims 1-56 and 80-100 were examined. Claims 1-56, 80-90 and 92-94 were rejected. Claims 91 and 95-100 were objected to but were indicated to contain allowable subject matter.

Applicants respectfully request reconsideration of the application in view of the amendments and remarks made herein.

No new matter has been added.

The Office Action

Claims Rejected Under 35 U.S.C. Section 112, Second Paragraph

In the Official Action of April 14, 2008, claim 88 was rejected under 35 U.S.C. Section 112, second paragraph as being indefinite. The Examiner asserted that a location has physical units while a score is dimensionless, and that it was unclear what is meant by the claimed distance in claim 88 and the units that it possesses. In response thereto, Applicants have amended claim 88 to clarify that the distances recited are distances measured between genetic location the genes represented by the gene related data that has been scored.

In view of the above amendment and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claim 88 under 35 U.S.C. Section 112, second paragraph as being indefinite, as being no longer appropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al.)

Claims 1-15 and 27-28 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-378) in view of Koleszar et al., U.S. Patent No. 6,519,583. The Examiner asserted that Ben-Dor et al. imports arbitrary RH data from the Whitehead institute as an external source, and uses identifiers in Table 4 to match them, as described in

lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372.

Applicants respectfully traverse. The markers of Table 4 are not arbitrary gene- or protein-related data, but are the identifiers that are used to locate positions on the chromosome, see page 365, column 1, last paragraph to page 365, column 2, second paragraph, and page 368, column 1, last paragraph to page 368, column 2, first paragraph. The Examiner, in the "Response to Arguments" section of the Office Action on page 10, asserted that, given the broad nature of the term "arbitrary gene- or protein-related data" that Ben-Dor et al. is interpreted to teach arbitrary genetic and protein related data because this broad term encompasses the genetic marker listed in Table 4 of Ben-Dor et al. which are related to genes. To clarify the distinction of the present invention over the markers of Ben-Dor et al., claim 1 has been amended to recite that, in addition to importing arbitrary gene- or protein-related data, an identifier is provided for each datum of said arbitrary gene- or protein-related data, wherein said identifiers specify genetic loci of said arbitrary gene- or protein- related data, respectively. Support for this amendment can be found, for example, at paragraph [0079] and throughout the specification. It is respectfully submitted that the Ben-Dor et al. does not additionally provide identifiers for locating the markers of Table 4, because the markers are the identifiers.

With regard to displaying the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map, Applicants reiterate that Ben-Dor et al. does not import arbitrary gene- or protein- related data as claimed. Further, with regard to the Examiner's assertion on page 10 of the Office Action that Bend-Dor et al. does display the predefined identifiers of Ben-Dor et al. adjacent to the identifiers of Ben-Dor et al. in Fig. 6, Applicants respectfully traverse. On the contrary, Fig. 6, shows the detailed differences between the two maps, see last line of page 371 to line 2 of page 372. Thus, for example, in the "first reversal" portion of Fig. 6 "CHLCGATAggCO5" in the WI map (left hand side), is not displayed adjacent "CHLCGATAggCO5" in the map of Ben-Dor et al. (right hand side). Rather, this entry appears near the bottom of the map on the left hand side, but appears near the top of the map on the right hand side. It is respectfully submitted that this cannot be properly interpreted to be "adjacent to" since every other entry in the WI map of this example is closer to "CHLCGATAggCO5" in the Ben-Dor et al. map than the "CHLCGATAggCO5" entry in the WI map.

It is further respectfully submitted that Koleszar et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and displaying the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located,

wherein all steps are automated steps, as claimed. Rather, Koleszar et al. teaches methods of graphically displaying computer-based biomolecular sequence information, which may be composed of nucleotide or amino acid sequence information, or both. Thus, Koleszar et al. appears to completely lack any disclosure of plotting this information adjacent chromosome maps. Nor does Ben-Dor et al. provide any teaching to map the information of Koleszar et al. adjacent a chromosome map. Accordingly, even if it would have been obvious to combine these references in the manner suggested by the Examiner, which Applicants do not agree that it would have been obvious, the resulting combination would still not meet all of the recitations of claim 1, for at least the reasons provided above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1-15 and 27-28 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-378) in view of Koleszar et al., U.S. Patent No. 6,519,583, as being inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al. and Stanyon et al.)

Claims 16, 18, 20-26, 29-33 and 55-56 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583, as applied to claims 1-15 and 27-28 above, and further in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155). The Examiner admitted that Ben-Dor et al. does not show expression matrices, statistical significance, additional information to the chromosome map, annotations, scores or statistical analyses of the matrices, but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of the homology study of Stanyon et al. because while Ben-Dor et al. examines difference in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determine similarities between the genomes of different species to aid in disease and genetic trait analyses.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data and provided identifiers as claimed, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located,

wherein all steps are automated steps, as claimed. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al., as specifically pointed out above.

It is further respectfully submitted that Stanyon et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Stanyon et al. teaches methods of painting probes to mouse and rat chromosomes , imaging the fluorescing probes, and then using a dual beam flow cytometer to sort chromosomes for DNA content. Figs. 3 and 4 are ideograms summarizing the hybridization results of the experiments of Stanyon et al. There is no disclosure or suggestion of generating these ideograms by the method recited in present claim 1. Further, the rat chromosomes are painted experimentally with mouse probes, and vice versa, and the comparisons are thus provided by directly analyzing the experimental data, not by reading an identifier associated with the data, matching it to a predefined identifier on a chromosome map and then overlaying the data on the chromosome map.

Nor does Stanyon teach or suggest displaying an expression matrix adjacent a chromosome map.

Although Applicants do not agree that it would have been obvious to combine the references as

suggested by the Examiner, since would have been no motivation to combine the references as suggested by the Examiner, even if the references were so combined, they would still fail to meet all of the recitations of the present claims since Stanyon et al. fails to make up for the deficiencies of Ben-Dor et al. and Koleszar et al. in meeting all of the recitations of claim 1.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 16, 18, 20-26, 29-33 and 55-56 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583, as applied to claims 1-15 and 27-28 above, and further in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155), as being inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al., Stanyon et al. and Singer et al.)

Claims 17 and 19 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583 and Stanyon et al. as applied to claims 1-16, 18, 20-33 and 55-56 above, and further in view of Singer et al. (U.S. Patent No. 5,866,331). The Examiner admitted that Ben-Dor et al. does not disclose the use of heat maps on a plurality of matrices, but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of Singer et al. by the use of heat maps because Singer et al. uses advanced mapping techniques to better detect hybridization to short sequences.

Applicants respectfully traverse. As noted above, it is respectfully submitted that neither Ben-Dor et al. nor Koleszar et al., nor Stanyon et al., whether taken alone or in any proper combination, imports arbitrary gene- or protein- related data and provides identifiers as claimed, reads the identifiers, matches the identifiers with predefined identifiers on at least one of the chromosome maps and displays the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps as claimed. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract. Koleszar et al. discloses methods for graphically displaying computer-based biomolecular sequence information, which may be composed of nucleotide or amino

acid sequence information, or both, and completely lacks any disclosure of plotting this information adjacent chromosome maps. Stanyon et al. is directed to methods of painting probes to mouse and rat chromosomes, imaging the fluorescing probes, and then using a dual beam flow cytometer to sort chromosomes for DNA content.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

It is further respectfully submitted that Singer et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Singer et al. merely teaches methods for accurately determining the total emission intensity of a single fluorochrome, under imaging conditions. Thus, Singer et al. appears to completely lack any disclosure of plotting this information adjacent chromosome maps. Nor does Ben-Dor et al. provide any teaching to map the information of Singer et al. adjacent a chromosome map. Accordingly, even if it would have been obvious to combine these references in the manner suggested by the Examiner, which Applicants do not agree that it would have been obvious, the resulting combination would still not meet all of the recitations of claim 1, for at least the reasons provided above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 17 and 19 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583 and Stanyon et al. as applied to claims 1-16, 18, 20-33 and 55-56 above, and further in view of Singer et al. (U.S. Patent No. 5,866,331), as being inappropriate.

Claim Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al. and Bodzin et al.)

Claim 80 was rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-378) in view of Koleszar et al., U.S. Patent No. 6,519,583 as applied to claims 1-15 and 27-28 above, and further in view of Bodzin et al., US Patent publication No. 2003/0139886). The Examiner asserted that claim 80 is drawing to the same subject mater as claim 1 with the additional limitation of dividing a microarray into a first control matrix and a second experimental matrix.

The Examiner asserted that Ben-Dor et al. imports arbitrary RH data from the Whitehead institute as an external source, and uses identifiers in Table 4 to match them, as described in lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372.

Applicants respectfully traverse. The markers of Table 4 are not arbitrary gene- or protein-related data, but are the identifiers that are used to locate positions on the chromosome, see page 365, column 1, last paragraph to page 365, column 2, second paragraph, and page 368, column 1, last paragraph to page 368, column 2, first paragraph. The Examiner, in the "Response to Arguments" section of the Office Action on page 10, asserted that, given the broad nature of the term "arbitrary gene- or protein-related data" that Ben-Dor et al. is interpreted to teach arbitrary genetic and protein related data because this broad term encompasses the genetic marker listed in Table 4 of Ben-Dor et al. which are related to genes. To clarify the distinction of the present invention over the markers of Ben-Dor et al., claim 80 has been amended like claim 1 to recite that, in addition to importing arbitrary gene- or protein-related data, an identifier is provided for each datum of said arbitrary gene- or protein-related data, wherein said identifiers specify genetic loci of said arbitrary gene- or protein- related data, respectively. Support for this amendment can be found, for example, at paragraph [0079] and throughout the specification. It is respectfully submitted that the Ben-Dor et al. does not additionally provide identifiers for locating the markers of Table 4, because the markers are the identifiers.

With regard to displaying the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map, Applicants reiterate that Ben-Dor et al. does not import arbitrary gene- or protein- related data as claimed. Further, with regard to the Examiner's assertion on page 10 of the Office Action that Bend-Dor et al. does display the predefined identifiers of Ben-Dor et al. adjacent to the identifiers of Ben-Dor et al. in Fig. 6, Applicants respectfully traverse. On the contrary, Fig. 6, shows the detailed differences between the two maps, see last line of page 371 to line 2 of page 372.

Thus, for example, in the "first reversal" portion of Fig. 6 "CHLCGATAggCO5" in the WI map (left hand side), is not displayed adjacent "CHLCGATAggCO5" in the map of Ben-Dor et al. (right hand side). Rather, this entry appears near the bottom of the map on the left hand side, but appears near the top of the map on the right hand side. It is respectfully submitted that this cannot be properly interpreted to be "adjacent to" since every other entry in the WI map of this example is closer to "CHLCGATAggCO5" in the Ben-Dor et al. map than the "CHLCGATAggCO5" entry in the WI map.

It is further respectfully submitted that Koleszar et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and displaying the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Koleszar et al. teaches methods of graphically displaying computer-based biomolecular sequence information, which may be composed of nucleotide or amino acid sequence information, or both. Thus, Koleszar et al. appears to completely lack any disclosure of plotting this information adjacent chromosome maps. Nor does Ben-Dor et al. provide any teaching to map the information of Koleszar et al. adjacent a chromosome map. Accordingly, even if it would have been obvious to combine these references in the manner suggested by the Examiner, which Applicants do not agree that it would have been obvious, the resulting combination would still not meet all of the recitations of claim 1, for at least the reasons provided above.

Still further, it is respectfully submitted that Bodzin et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and displaying the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Bodzin et al. discloses multiplexing analysis software used to deconvolve and normalize colored assay data. Since Ben-Dor et al. does not appear to disclose use of colored assay data, it is respectfully submitted that there would have been no motivation to combine Bodzin et al. with Ben-Dor et al. Even if the references were combined as suggested by the Examiner, they would still fail to meet all of the limitations of claim 80, since Bodzin et al. fails to make up for the deficiencies of Ben-Dr et al. and Koleszar et al. for at least the reasons provided above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claim 80 under 35 U.S.C. Section 103(a) as being unpatentable

over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-378) in view of Koleszar et al., U.S. Patent No. 6,519,583 as applied to claims 1-15 and 27-28 above, and further in view of Bodzin et al., US Patent publication No. 2003/0139886, as being inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al., Stanyon et al. and Bodzin et al.)

Claims 81-83, 85-87, 90 and 93-94 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583, and in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155) as applied to claims 1-16, 18, 20-33 and 55-56 above, and further in view of Bodzin et al., US Patent Publication No. 2003/0139886. The Examiner admitted that Ben-Dor et al. does not show expression matrices, statistical significance, additional information to the chromosome map, annotations, scores or statistical analyses of the matrices, but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of the homology study of Stanyon et al. because while Ben-Dor et al. examines difference in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determine similarities between the genomes of different species to aid in disease and genetic trait analyses.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data and provided identifiers as claimed, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any

chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al., as specifically pointed out above.

It is further respectfully submitted that Stanyon et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Stanyon et al. teaches methods of painting probes to mouse and rat chromosomes , imaging the fluorescing probes, and then using a dual beam flow cytometer to sort chromosomes for DNA content. Figs. 3 and 4 are ideograms summarizing the hybridization results of the experiments of Stanyon et al. There is no disclosure or suggestion of generating these ideograms by the method recited in present claim 1. Further, the rat chromosomes are painted experimentally with mouse probes, and vice versa, and the comparisons are thus provided by directly analyzing the experimental data, not by reading an identifier associated with the data, matching it to a predefined identifier on a chromosome map and then overlaying the data on the chromosome map.

Nor does Stanyon et al. teach or suggest displaying an expression matrix adjacent a chromosome map.

Although Applicants do not agree that it would have been obvious to combine the references as suggested by the Examiner, since would have been no motivation to combine the references as suggested by the Examiner, even if the references were so combined, they would still fail to meet all of the recitations of the present claims since Stanyon et al. fails to make up for the deficiencies of Ben-Dor et al. and Koleszar et al. in meeting all of the recitations of claim 80.

Still further, Still further, it is respectfully submitted that Bodzin et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome

maps and displaying the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Bodzin et al. discloses multiplexing analysis software used to deconvolve and normalize colored assay data. Since Ben-Dor et al. does not appear to disclose use of colored assay data, it is respectfully submitted that there would have been no motivation to combine Bodzin et al. with Ben-Dor et al. Even if the references were combined as suggested by the Examiner, they would still fail to meet all of the limitations of claim 80, since Bodzin et al. fails to make up for the deficiencies of Ben-Dor et al., Koleszar et al. and Stanyon et al. for at least the reasons provided above.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 81-83, 85-87, 90 and 93-94 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583, and in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155) as applied to claims 1-16, 18, 20-33 and 55-56 above, and further in view of Bodzin et al., US Patent Publication No. 2003/0139886), as being inappropriate.

Claims Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al., Stanyon et al., Bodzin et al. and McCully)

Claims 84 and 89 were rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583, in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155) and in view of Bodzin et al., US Patent Publication No. 2003/0139886, as applied to claims 1-16, 18, 20-33 and 55-56, 81-83, 85-87, 90 and 93-94 above, and further in view of McCully, U.S. Patent No. 4,383,994.

The Examiner admitted that Ben-Dor et al. does not show expression matrices, statistical significance, additional information to the chromosome map, annotations, scores or statistical analyses of the matrices, but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of the homology study of Stanyon et al. because while Ben-Dor et al. examines difference in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determine similarities between the genomes of different species to aid in disease and genetic trait analyses.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data and provided identifiers as claimed, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al., as specifically pointed out above.

It is further respectfully submitted that Stanyon et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Stanyon et al. teaches methods of painting probes to mouse and rat chromosomes , imaging the fluorescing probes, and then using a dual beam flow cytometer to sort chromosomes for DNA content. Figs. 3 and 4 are ideograms summarizing the hybridization results of the experiments of Stanyon et al. There is no disclosure or suggestion of generating these ideograms by the method recited in present claims 1 and 80. Further, the rat

chromosomes are painted experimentally with mouse probes, and vice versa, and the comparisons are thus provided by directly analyzing the experimental data, not by reading an identifier associated with the data, matching it to a predefined identifier on a chromosome map and then overlaying the data on the chromosome map.

Nor does Stanyon et al. teach or suggest displaying an expression matrix adjacent a chromosome map.

Although Applicants do not agree that it would have been obvious to combine the references as suggested by the Examiner, since would have been no motivation to combine the references as suggested by the Examiner, even if the references were so combined, they would still fail to meet all of the recitations of the present claims since Stanyon et al. fails to make up for the deficiencies of Ben-Dor et al. and Koleszar et al. in meeting all of the recitations of claim 80.

Still further, Still further, it is respectfully submitted that Bodzin et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and displaying the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Bodzin et al. discloses multiplexing analysis software used to deconvolve and normalize colored assay data. Since Ben-Dor et al. does not appear to disclose use of colored assay data, it is respectfully submitted that there would have been no motivation to combine Bodzin et al. with Ben-Dor et al. Even if the references were combined as suggested by the Examiner, they would still fail to meet all of the limitations of claim 80, since Bodzin et al. fails to make up for the deficiencies of Ben-Dor et al., Koleszar et al. and Stanyon et al. for at least the reasons provided above.

Still further, McCully is directed to use of salts as neoplastic agents, as admitted by the Examiner, and has nothing whatsoever to do with overlaying gene- or protein-related data on chromosome maps. Accordingly, even if it would have been obvious to combine McCully with the other references as suggested by the Examiner, which Applicants do not agree that it would have been obvious, since McCully is totally unrelated to the disclosures of the other references, McCully would still fail to make up for the deficiencies of the other references in meeting all of the recitations of claim 80.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 84 and 89 under 35 U.S.C. Section 103(a) as being

unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583, in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155) and in view of Bodzin et al., US Patent Publication No. 2003/0139886, as applied to claims 1-16, 18, 20-33, 55-56, 81-83, 85-87, 90 and 93-94 above, and further in view of McCully, U.S. Patent No. 4,383,994, as being inappropriate.

Claim Rejected Under 35 U.S.C. Section 103(a) (Ben-Dor et al. in view of Koleszar et al., Stanyon et al., Bodzin et al. and Anton)

Claim 92 was rejected under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583, in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155) and in view of Bodzin et al., US Patent Publication No. 2003/0139886, as applied to claims 1-16, 18, 20-33 m 55-56, 81-83, 85-87, 90 and 93-94 above, and further in view of Anton, Elementary Linear Algebra, John Wiley and Sons: New York, 1987, pages 12-127.

The Examiner admitted that Ben-Dor et al. does not show expression matrices, statistical significance, additional information to the chromosome map, annotations, scores or statistical analyses of the matrices, but asserted that it would have been obvious to modify the radiation hybrid ordering method of Ben-Dor et al. in view of the homology study of Stanyon et al. because while Ben-Dor et al. examines difference in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determine similarities between the genomes of different species to aid in disease and genetic trait analyses.

Applicants respectfully traverse. As noted above, it is respectfully submitted that Ben-Dor et al. does not import arbitrary gene- or protein- related data and provided identifiers as claimed, read the identifiers, match the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Ben-Dor et al. is a method for ordering markers along a chromosome and estimating the physical distances between them, see page 365, column 1, lines 5-7 of the first paragraph after the abstract.

Ben-Dor et al. irradiates cells to break chromosomes at random locations into separate fragments, wherein the fragments are subintervals of the original chromosomes and contain markers. A

random subset of the fragments is rescued, and an algorithm is used to deduce the most likely linear order of the markers on the chromosome, based on the retention pattern of the markers in the retained fragments (having been cloned) and estimating the spacing between the markers. Thus, any chromosome plot showing markers is not plotted by looking up identifiers for the markers and then placing the markers adjacent a chromosome map having the predefined identifiers thereon, but the placement and spacing of the markers is determined by the algorithmic process described by Ben-Dor et al.

Fig. 6 of Ben-Dor et al., which was referred to by the Examiner, simply shows differences between the mapping technique of Ben-Dor et al. and that of the WI framework map, it is not the result of an automated process to map arbitrary gene- or protein-related data to a chromosome map. Nor are the numbers of the WI framework map displayed adjacent the matching numbers on the Ben-Dor et al., as specifically pointed out above.

It is further respectfully submitted that Stanyon et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and display the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Stanyon et al. teaches methods of painting probes to mouse and rat chromosomes , imaging the fluorescing probes, and then using a dual beam flow cytometer to sort chromosomes for DNA content. Figs. 3 and 4 are ideograms summarizing the hybridization results of the experiments of Stanyon et al. There is no disclosure or suggestion of generating these ideograms by the method recited in present claims 1 and 80. Further, the rat chromosomes are painted experimentally with mouse probes, and vice versa, and the comparisons are thus provided by directly analyzing the experimental data, not by reading an identifier associated with the data, matching it to a predefined identifier on a chromosome map and then overlaying the data on the chromosome map.

Nor does Stanyon et al. teach or suggest displaying an expression matrix adjacent a chromosome map.

Although Applicants do not agree that it would have been obvious to combine the references as suggested by the Examiner, since would have been no motivation to combine the references as suggested by the Examiner, even if the references were so combined, they would still fail to meet all of the recitations of the present claims since Stanyon et al. fails to make up for the deficiencies of Ben-Dor

et al. and Koleszar et al. in meeting all of the recitations of claim 80.

Still further, Still further, it is respectfully submitted that Bodzin et al. also fails to teach or suggest importing arbitrary gene- or protein- related data and providing identifiers as claimed, reading the identifiers, matching the identifiers with predefined identifiers on at least one of the chromosome maps and displaying the arbitrary gene- or protein- related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein all steps are automated steps, as claimed. Rather, Bodzin et al. discloses multiplexing analysis software used to deconvolve and normalize colored assay data. Since Ben-Dor et al. does not appear to disclose use of colored assay data, it is respectfully submitted that there would have been no motivation to combine Bodzin et al. with Ben-Dor et al. Even if the references were combined as suggested by the Examiner, they would still fail to meet all of the limitations of claim 80, since Bodzin et al. fails to make up for the deficiencies of Ben-Dor et al., Koleszar et al. and Stanyon et al. for at least the reasons provided above.

Still further, Anton is simply directed to matrix manipulations and has nothing whatsoever to do with overlaying gene- or protein-related data on chromosome maps. Accordingly, even if it would have been obvious to combine Anton with the other references as suggested by the Examiner, which Applicants do not necessarily agree that it would have been obvious, Anton would still fail to make up for the deficiencies of the other references in meeting all of the recitations of claim 80.

In view of the above amendments and remarks, the Examiner is respectfully requested to reconsider and withdraw the rejection of claim 92 under 35 U.S.C. Section 103(a) as being unpatentable over Ben-Dor et al. (Genome Research, 2000, volume 10, pages 365-278) in view of Koleszar et al., U.S. Patent No. 6,519,583, in view of Stanyon et al. (Cytogenics and Cell Genetics, volume 84, 1999, pages 150-155) and in view of Bodzin et al., US Patent Publication No. 2003/0139886, as applied to claims 1-16, 18, 20-33 m 55-56, 81-83, 85-87, 90 and 93-94 above, and further in view of Anton, Elementary Linear Algebra, John Wiley and Sons: New York, 1987, pages 12-127, as being inappropriate.

New Claim101

Claims 91 and 95-100 were objected to as being dependent upon a rejected base claim, but the Examiner indicated that these claims would be allowable if rewritten into independent form to include

all of the limitations of the base claim and any intervening claims.

In response thereto, Applicants have submitted new independent claim 101 above. Claim 101 combines the recitations of claims 80 (prior to the above amendment of claim 80), 90 and 91. Accordingly, the Examiner is respectfully requested to indicate the allowance of claim 101 in the next Official Action.

Claim 91 has been canceled above, without prejudice, and claim 95 has been amended to depend from claim 101. Accordingly, the Examiner is respectfully requested to indicate the allowance of claims 95-100 in the next Official Action.

Conclusion

Applicants submit that all of the claims are in condition for allowance, which action is requested. If the Examiner finds that a telephone conference would expedite the prosecution of this application, please telephone the undersigned at the number provided.

The Commissioner is hereby authorized to charge any underpayment of fees associated with this communication, including any necessary fees for extensions of time, or credit any overpayment to Deposit Account No. 50-1078, order number 10020503-2.

Respectfully submitted,

Date: 7/18/08

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